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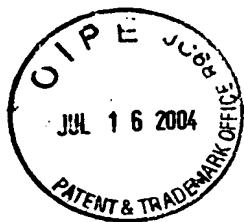
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1/27

48 KD G1 i-antigen : protein and nucleic acid sequences

[illegible]

Fig. 1

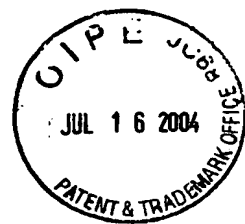
REPLACEMENT SHEET

2/27

G5 Wild-type

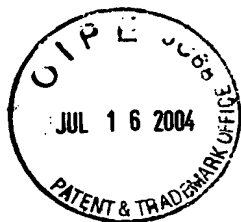
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130 140 150 160 170 180 190 200 210 220 230 240
CCGCAAAAT GTGTAAATG TTAGAAAAC TTTTATTATA ATAAATCTGC TGCTTTGGTT CCTGGTGCTA GTACGTGTAC ACCTTGTCCT TAAAAAAAAG ATGCTGGTGC TTAACCAAAAT
250 260 270 280 290 300 310 320 330 340 350 360
CCACCTGTCA CTGCTAATTT AGTCACATAA TCTAAGGTTA AATGCCCTGC TGGTACCGCA ATTGCAGGTG GAGCAACAGA TTATGCCAGCA ATATCAACAG AATGTGTTAA TTGTAGAAAT
370 380 390 400 410 420 430 440 450 460 470 480
AATTTTATA ATGAANAATC TCCAAATTTT AATGCAGGTG CTATGATGATG GAGTGTGCTG TGCATTTGACT GCTGGTAAATG CCGCTACCAT AGTCCGATTA
490 500 510 520 530 540 550 560 570 580 590 600
TGTACGCTCG CATGTCTTAC TGGTACTGCA CTGTGATGATG GAGTACTACT TGAATATGTT AGATCAATCA CAGAAATGCT TAAATGTAGA CTTAACCTTTT ACTATAATGG TAATAATGCT
610 620 630 640 650 660 670 680 690 700 710 720
AATATCTCTT TCAATCCAGG TAAAGTTTAA TCCACACCTT TCCACACCTT TAAACCTGCT AATGTGCTT TGTACTAATTT GTGCTCTTAA CTTTTCACAT AATAATGCTC CTAAATTTCAA TCCAGGTAAT
730 740 750 760 770 780 790 800 810 820 830 840
TCCCTGATG GTACTATATG TGCCTGCTGA GTAAATATTT GGSTAGCACA AAACACTGAA TGTACTAATTT TAGCTCTTAA CTTTTCACAT AATAATGCTC CTAAATTTCAA TCCAGGTAAT
850 860 870 880 890 900 910 920 930 940 950 960
AGTACATGCC TACCTTGCCC AGCAATAAAA GATTATGCTG CTGAAGCCAC TGCAGGTGCT GCGCTACTT TAGCCCAATA ATGTAAATAT GCATGCCCTG ATGGTACTGC AATTGCTACT
970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
GGAGCACTA ATTATGTAAT ATTATTAACA GAATGCTTAA ATTGTGCTG TAACTTTTAT TTGTAGGCTA ATAAATTTCTA GGCAGGAAGT AGTAGATGCA AAGCATGTGC AGCAATAAA
1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
GTTTAAAGCG CTGTACCAAC TGCAGGTGCT ACTGCTACTT TAATTTGCTA ATGTGCTT GAATGCCCTG CTGGTACTGT ACTCACCGAT GGAACAACAT CTACTTTATA ATTAAGCGCA
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
TCTGAATGCG TTAATGTCGC TGCCAACTTT TATACTACAA AATAAAGTCA TTGGTAGCA GGTATGATCA CATGTACTAG TTGTAAATAA AATTAACCTT CTGGCGCTGA AGCTAATTTA
1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
CCTGAATCTG CTAAAAAAA TATATAATGT GATTTGGCTA ATTTTATC AATTTCCTTA TTATTTATTT CTATTAATTT ATTAATGATGA
Coding region: nucleotides 1-1404

Fig. 2a



REPLACEMENT SHEET

3/27



G5 SYNTHETIC

10	20	30	40	50	60	70	80	90	100	110	120
ATGAAGAACA	ACATCTCTGT	GATCCTGTATC	ATCTCTCTGT	TCATCAACCA	GATCAAGTCT	GCTAACTGTC	CTGTGGGAAC	CGAGACCAAC	ACCCTGGAC	AGGTGGACGA	CCTGGGAACC
130	140	150	160	170	180	190	200	210	220	230	240
CCTGCTAACT	GTGTGAACCTG	TCAGAAGAAC	TTCTACTACA	ACAACGCTGC	TGCTTTGGTG	CCTGGAGCTT	CTAACCTGTAC	CCCTTGCTCT	CAGAAGGAGG	ACGCTGGAGC	TCAGCCTAAC
250	260	270	280	290	300	310	320	330	340	350	360
CCTCTCTGTA	CCGCTAACT	GGTGAACCCAG	TGTAACTGA	AGTGTCTCTG	TGGAACCGCT	ATCCTCTGAG	GAGCTAACGA	CTAACGCTGCT	ATCATCAACG	AGTGTGTGAA	CTGTGCGATC
370	380	390	400	410	420	430	440	450	460	470	480
AACCTCTACA	ACGAGAACGC	TCTTAACCTC	AACGCTGAG	CTTCTAACCTG	TACCGCTTGT	CCTGTGAACC	GGCTGGAGG	AGCTCTGACC	GCTGGAACCG	CTGTACCACT	CGTGGCTCAG
490	500	510	520	530	540	550	560	570	580	590	600
TGTAAAGTGG	CTTGTCTTAC	CGGAACCGCT	CTGGAACGAG	GAGTGACAC	CGACTAAGTG	CGCTCTTTTCA	CCGAGTGTGT	GAGGTGTGCG	CTGAACCTTCT	ACTACAAACGG	AAACAACGGA
610	620	630	640	650	660	670	680	690	700	710	720
AACACCCCTT	TCAACCCCTG	AAAGTCTCAG	TGTAAACCTG	GTCTGTCTAT	CAAGCCTGCT	AACGTGCTC	AGGCTAACCT	GGGAAACGAC	GCTACCAATCA	CCGCTCAGTG	TAACTGTGCT
730	740	750	760	770	780	790	800	810	820	830	840
TGTCTGACG	GAACCATCTC	TGCTGCTGGA	GTGAACCACT	GGGTGGCTCA	GAACACCGAG	TGTAAACCACT	GTGCTCTTAA	CTTCTTACAC	AACAACGCTC	CTAACCTTCA	CCCTGGAAAC
850	860	870	880	890	900	910	920	930	940	950	960
TCTAACCTGC	TGCTTGTGTC	TGCTTAACAG	GACTAAGGAG	CTGAGGCTAC	CGCTGGAGGA	GCTCTAACCC	TGGCTAAGCA	GTGTAAACATC	GCTTGTCTCTG	ACGGAAACGC	TATGTGCTCT
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
GGAGCTAACCA	ACTAAGTGAT	CCTGAGACCC	GAGTGTCTGA	ACTGTGCTGC	TAACTTCTTAC	TTTGAACGGA	ACAACCTTCCA	GGCTGTGATCT	TCTGTGCTGTA	AGGCTTGTCC	TGCTTAACAG
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
GTGCAGGGAG	CTGTGGCTAC	CGCTGGAGGA	ACCCTTAACC	TGATCGCTCA	GTGTGCTCTG	GAGTGTCTCTG	CTGGAAACCGT	GCTGAACCGAC	GGAAACCACT	CTAACCTTAA	GCAGGCTGCT
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
TCTGAGTGTG	TGAAAGTGTG	TGCTTAACCTC	TACACCAACCA	AGCAGACCGA	CTGGGTGGCT	GGATGTGACA	CCTGTACTCTC	TTGTAAACAG	AAGCTGACT	CTGGAGCTGA	GGCTTAACCTG
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
CCTGAGTCTG	CTAAGAGAA	CATCCAGTGT	GACTTGCTTA	ACTTCTCTGC	TATCTCTCTG	CTGTGATCT	CTTACTACT	GCTGTATTA

Coding region: nucleotides 1-1404

Fig. 2b



4/27

Sequence Alignment of 48 kD G1 i-antigen and 55 kD G5 i-antigen protein sequences

[illegible]

Fig. 3a

REPLACEMENT SHEET

5/27

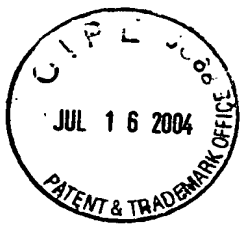


Fig. 3b₁

Fig. 3b₂

Fig. 3b

REPLACEMENT SHEET

6/27

Fig. 3b₁

Sequence Alignment of 48 kD G1 i-antigen and 55 kD G5 i-antigen nucleotide sequences

[illegible]



7/27

G1 ATGTCCTACTGGCACTGTACTTGATGATGGAGTGACACTTGT TTTTAATACATCAGCCAC
G5 ATGTCCTACTGGTACTGCACCTTGATGATGGAGTAACTACTGATTATGTTAGATCATTAC
***** ** * * * * *

G1 ATTATGTGTTAAATGCAGACCTAACTTTTACTATAATGGT-----GGTT---CTCCTTA
G5 AGAATGTGTTAAATGTAGACTTAACTTTTACTATAATGGTAATAATGGTAATACTCCTTT
* ***** ** *

G1 -----AGGTGAA-----GCTCCTGGCGTTTA
G5 CAATCCAGGTAAAGTTAATGCACACCTTGTCGGCAATTAAACCTGCTAATGTTGCTTA
***** ** *

G1 AG-----TTT-----TTGC-----TGCTGG
G5 AGCTACTTTAGGTAATGATGCTACAATAACCGCATAATGTAACGTTGCATGCCCTGATGG
** *** **** ** *

G1 TGCT-----GCCGCTGCAG-----GTGTTGC-----
G5 TACTATAAGTGCTGCTGGAGTAAATAATTGGGTAGCACAAAACACTGAATGTACTAATTG
* ** * * * *

G1 -----TGCCGTTACTAGTTAATGTGT
G5 TGCTCCTAACTTTTACAATAATAATGCTCCTAATTTCAATCCAGGTAAATAGTACATGCCT
* * * * *

G1 ACCTTGCCAAATAAAACAAAACGATTCTCCTG---CCACTGCAGGTGCCAAGCTAATTT
G5 ACCTTGCCAGCAATAAAGATTATGGTGCTGAAGCCACTGCAGGTGGTGCCGCTACTTT
***** * * * * *

G1 AGCCACATAATGCAGTACTTAATGTCCAACCTGGCACTGCAATT-CAAGACGGAGTGACAC
G5 AGCCAAATAATGTAATATTGCATGCCCTGATGGTACTGCAATTGCTAGT-GGAGCAAC--
***** * * * * *

G1 TTGTTTTTAGTAAT-TCATCCACATAATGTCTTAAT-GCATTGCTAATTACTTTTTTAA
G5 -TAATTAT-GTAATATTATAACAGAAATGT-CTAAATTGTGCTGCTAACTTTTATTTTGA
* * * * *

G1 TGGTAAT---TTCGAAGCAGGTAAAAGTTAATGTTTAAAG--TGTCCAGTAAGTAAACT
G5 TGGTAATAATTTCTAGGCAGGAAGTAGTAGATGC--AAAGCATGTCCAGCAAAATAAGTT
***** * * * * *

G1 A-----CTCCAGCACATGCTCCAGGTAATACTGCTACTTAAAGCCACATAATGT---TT
G5 TAAGGCGCTGTAGCAA---CTGCAGGTGGTACTGCTACTTTAATTGCATAATGTGCCCTT
** ***** ** *

G1 GACCACATGTCCTGCTGGTACAGTACTTGATGATGGAACATCAACTAATTTGTAGCTTC
G5 GA---ATGCCCTGCTGGTACTGTACTCACCAGTGAACAACATCTACTTATAAATAAGC
** * * * * *

G1 CGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTCATCAAAAACAACTGGTTTAC
G5 AGCATCTGAATGTGTTAAATGTGCTGCCAACTTTTATACTACAAAATAAAGTATGGGT
* * * * *

G1 AGCAGGTACTGATACATGTACTGAATGTACTAAAAAATTAACCTCTGGTGCCACAGCTAA
G5 AGCAGGTATTGATACATGTACTAGTTGTAATAAAAAATTAACCTCTGGCGCTGAAGCTAA
***** ** *

G1 AGTATATGCTGAAGCTACTCAAAAAG---TATAATGCGCCTCCACTACTTTCGCTAAATT
G5 TTTAC---CTGAATCTGCTAAAAAATATATAATGTG-----ATTTCGCTAATTT
* * * * *

G1 TTTATCGATTTCTTATTATTATTCTTTCTATTATTG
G5 TTTATCAATTTCTTATTATTGATTTCTTATTATTATTA

Fig. 3b₂

8/27



55 KD i-antigen protein

SEQ ID NO: 7	10	20	30	40	50	60
	MKNNILVILI	ISLFINQIKS	ANCPVGTETN	TAGQVDDLGT	PANCVNCQKN	FYYNNAAAFV
	70	80	90	100	110	120
	PGASTCTPCP	QKKDAGAQP	PPATANLVTQ	CNVKCPAGTA	IAGGATDYAA	IITECVNCRI
	130	140	150	160	170	180
	NFYNENAPNF	NAGASTCTAC	PVNRVGGALT	AGNAATIVAQ	CNVACPTGTA	LDDGVTTDYV
	190	200	210	220	230	240
	RSFTECVKCR	LNFYNGNG	NTPFNPQKSQ	CTPCPAIKPA	NVAQATLGND	ATITAQCIVA
	250	260	270	280	290	300
	CPDGTISAAG	VNNWVAQNT	CTNCAPNFYN	NNAPNFNPGN	STCLPCPANK	DYGAEATAGG
	310	320	330	340	350	360
	AATLAKQCNI	ACPDGTALAS	GATNYVILQT	ECLNCAANFY	FDGNNFQAGS	SRCKACPANK
	370	380	390	400	410	420
	VQGAVATAGG	TATLIAQCAL	ECPAGTVLTD	GTTSTYKQAA	SECVKCAANF	YTTKQTDWVA
	430	440	450	460	470	480
	GIDTCTSCNK	KLTSGAEANL	PESAKKNIQC	DFANFLSISL	LLISYLL**

Fig. 4



9/27

48 KDa G1 i-antigen repeats

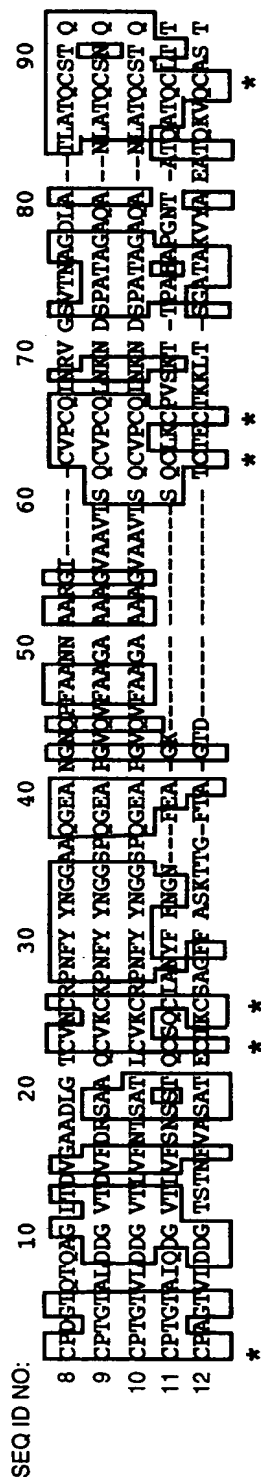


Fig. 5a

55 kDa G5 i-antigen repeats

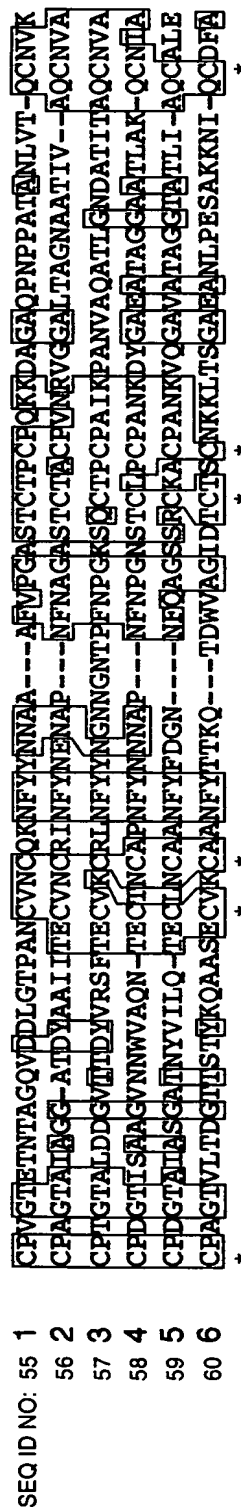


Fig. 5b

10/27

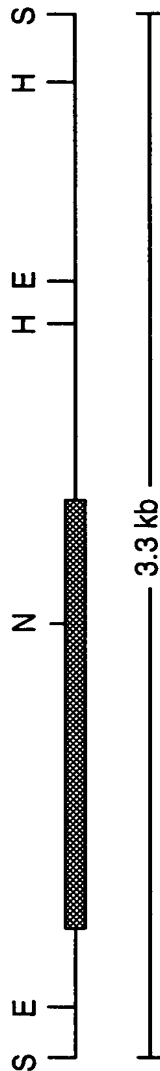


Fig. 6

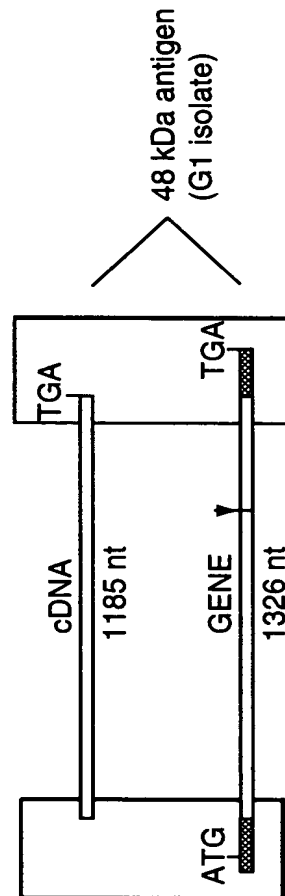


Fig. 7a



Diagram illustrating the structure of the human PTPN11 gene and cDNA. The gene structure shows exons (1, 56, 1227) and introns. The cDNA structure shows the coding sequence with start (ATG) and stop (TGA) codons. The protein structure shows the protein sequence with start (M) and stop (F) codons. The protein is 1172 amino acids long.

Fig. 7b

[illegible]

Fig. 7c



12/27

SEQ ID NO: 61 i-ag
SEQ ID NO: 62 vspA6-S1
20 AVFDPDGTQTOAG-LTDVGAADLGTVCNCRPNFYNGGAAGQ---EANGNP-FAANNAAR--GICVP---CQINRVGSVTNAGDLATL
61 AVICDQ---GSAGYTDSDSVDAKECKCKCNAPCTACAGTADKCTKCDANGAPYLKKNPSPDPTGICVSAVIDCG-SAGYTT--DDSVSD
* * * * *
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
ATQSTQCPGTGALTDDGVTVDRSAACVCKCPN-----FYNGGSPQ-GE-----APGVQVFAAGAAAGVAAVTSQCVFCOLKNKNDSPA
AKECK-RCLEGOKPNTAGTQCTSCSDANCERCDONDVCAKSTGAPPENKCPAATPGCHSDDGCTENAMTNQADNCKGCKEGRYLKPE
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
TAGAQANLATQCSNCPGTGTVLDDGVTVLVENTSATLCTVCRPNFYNGGSPQGEAPGVQVFAAGAAAGVAAVTSQCVFCOLKNKNDSPAT
SAAGQSGTCLT-AEBCSTDTTE--FTKEKAGDSKGMCLFCS-----DATHGIAGCKK--CAL---KTLGGEAESTVVCBEC-TDKWLTPS-
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
AGAQANLATQCSNCPGTGTALQDGVTVLFSNSSTQCSCLANTFFNGNFEAGKSQCLCPVSKTTPAHAPGNATATQCLTTP--AGT
-G----N---HCLDNCPAGTYFND-NNLCTSCHDT-CBEC-----NGN--ADRAQTAC-----YPCVSLLYGSGCTAGTCVKECTGAFGA
* * * * *
* * * * *
* * * * *

i-ag
vspA6-S1
VLDDGTSTNFWASATECTNCSAGFP-----ASKTTGFT-----AGTD--TCTECTTKLTSGATAKVY--AEATQKVQCBSTTPAK 428
NCADGQCTADVGGAKYCAQCKEDGYAPIDGICTAVAAAGRTNVCTAADGTCTKCAGEYT-LMSGGCGYVAKLPCKSVCTLASNGK 459
* * * * *
* * * * *
* * * * *

Fig. 8



13/27

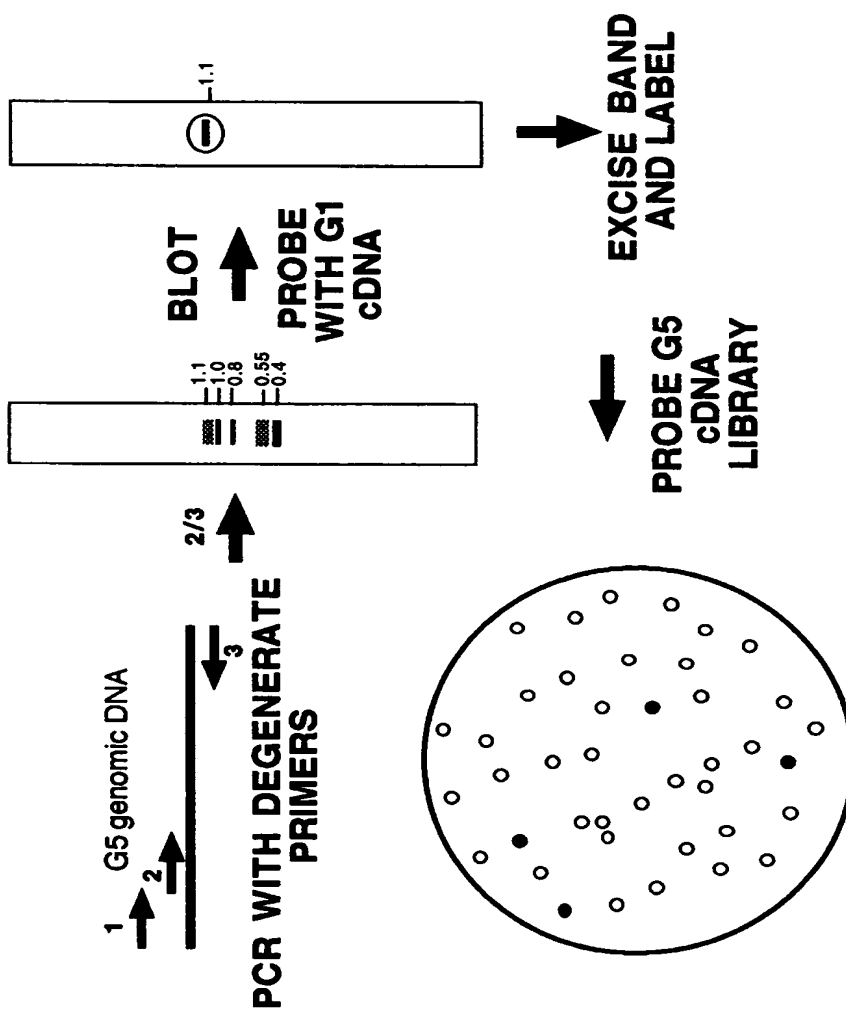


Fig. 9

REPLACEMENT SHEET

14/27

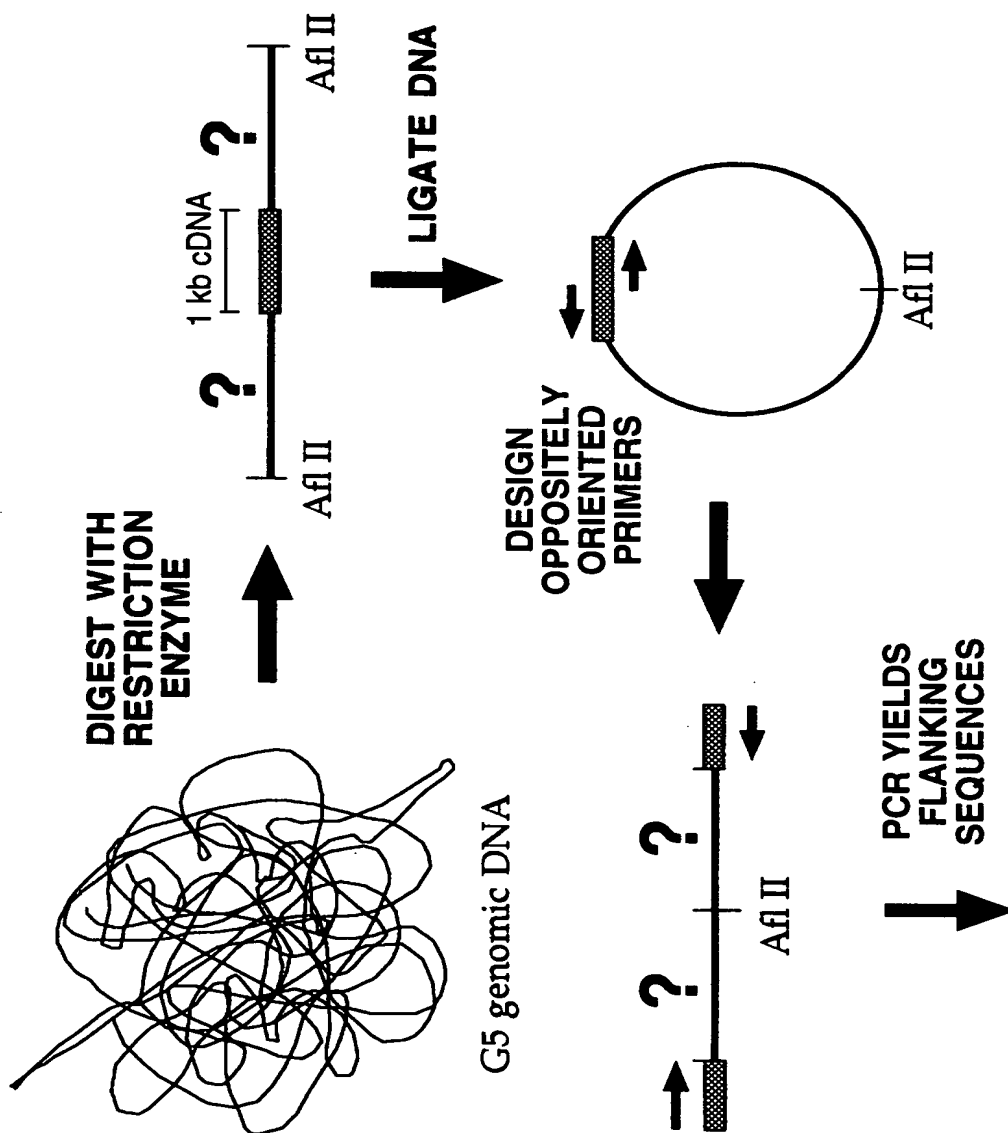


Fig. 10

REPLACEMENT SHEET

15/27

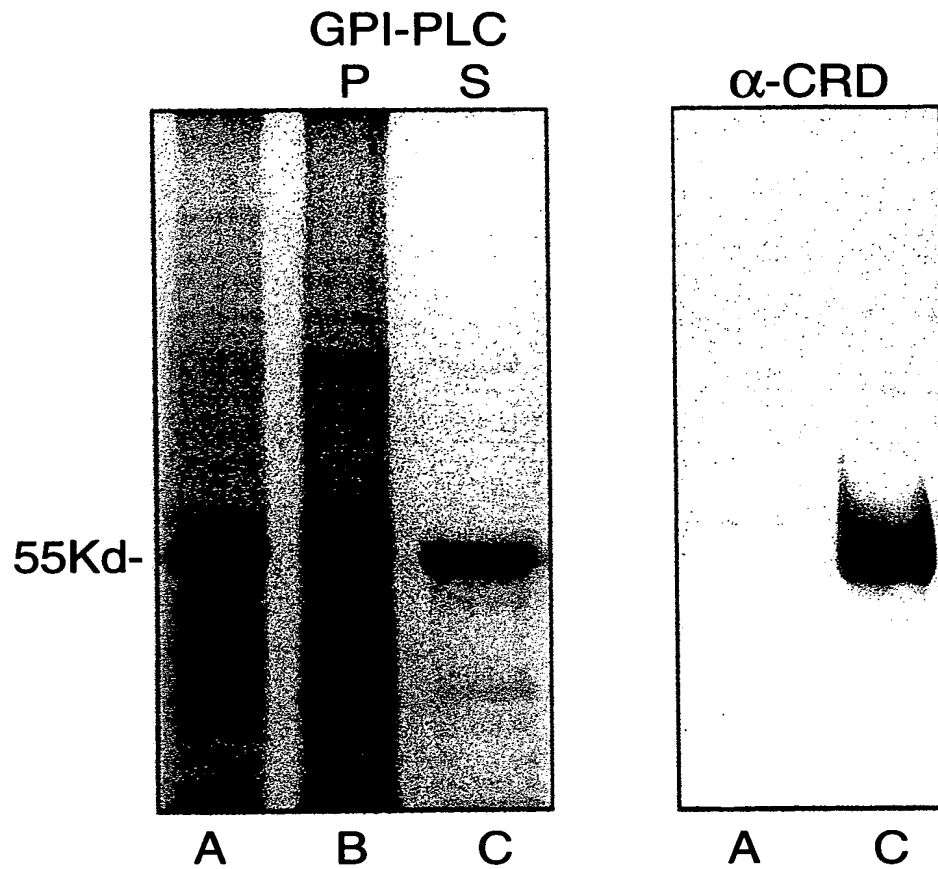


Fig. 11

REPLACEMENT SHEET

16/27



SEQ ID NO: Primers for synthesis of G5 synthetic gene.

- 3201:
70 ATG GGA ATT CAA ATG AAG AAC AAC ATC CTG GTG ATC CTG ATC ATC TCT CTG TTC ATC AAC CAG ATC AAG
TCT GCT AAC TGT OCT GTG GGA ACC GAG ACC AAC ACC GCT GGA CAG GTG
- 3202:
71 CTC CAG GCA CGA AAG CAG CAG CGT TGT TGT AGT AGA AGT TCT TCT GAC AGT TCA CAC AGT TAG CAG GGG
TTC CCA GGT CGT CCA CCT GTC CAG CGG TGT TGG TC
- 3203:
72 CGC TGC TGC TTT CGT GCC TGG AGC TTC TAC CTG TAC CCC TTG TCC TCA GAA GAA GGA CGC TGG AGC TCA
GCC TAA CCC TCC TGC TAC CGC TAA CCT GGT G
- 3204:
73 GAT GAT AGC AGC GTA GTC GGT AGC TCC AGC GAT AGC GGT TCC AGC AGG ACA CTT CAC GTT ACA CTG
GGT CAC CAG GTT AGC GGT AGC AGG AG
- 3205:
74 GCT ACC GAC TAC GCT GCT ATC ATC ACC GAG TGT GTG AAC TGT CGC ATC AAC TTC TAC AAC GAG AAC GCT
CCT AAC TTC AAC GCT GGA GCT TCT ACC TGT ACC GCT TGT OCT GTG AAC CGC GTG GGA GGA GCT CTG ACC
- 3206:
75 GGT GAA AGA GCG CAC GTA GTC GGT GGT CAC TCC GTC GTC CAG AGC GGT TCC GGT AGG ACA AGC CAC GTT
ACA CTG AGC CAC GAT GGT AGC AGC GTT TCC AGC GGT CAG AGC TCC TCC CAC GCG
- 3207:
76 GAC TAC GTG CGC TCT TTC ACC GAG TGT GTG AAG TGT CGC CTG AAC TTC TAC TAC AAC GGA AAC AAC GGA
AAC ACC CCT TTC AAC CCT GGA AAG TCT CAG
- 3208:
77 GTG ATG GTA GCG TCG TTT CCC AGG GTA GCC TGA GCC ACG TTA GCA GGC TTG ATA GCA GGA CAA GGG GTA
CAC TGA GAC TTT CCA GGG TTG AAA GG
- 3209:
78 GGG AAA CGA CGC TAC CAT CAC CGC TCA GTG TAA CGT GGC TTG TCC TGA CGG AAC CAT CTC TGC TGC TGG
AGT GAA CAA CTG GGT GGC TCA GAA C
- 3210:
79 CAG ACA GGT AGA GTT TCC AGG GTT GAA GTT AGG AGC GTT GTT GTT GTA GAA GTT AGG AGC ACA GTT GGT
ACA CTC GGT GTT CTG AGC CAC CCA GTT GTT C
- 3211:
80 CCC TGG AAA CTC TAC CTG TCT GGC TTG TCC TGC TAA CAA GGA CTA CGG AGC TGA GGC TAC CGC TGG AGG
AGC TGC TAC OCT GGC TAA GC
- 3212:
81 GGT CTG CAG GAT CAC GTA GTT GGT AGC TCC AGA AGC GAT AGC GGT TCC GTC AGG ACA AGC GAT GTT ACA
CTG CTT AGC CAG GGT AGC AGC
- 3213:
82 CAA CTA CGT GAT CCT GCA GAC CGA GTG TCT GAA CTG TGC TGC TAA CTT CTA CTT CGA CGG AAA CAA CTT
CCA GGC TGG ATC TTC TCG CTG TAA GG
- 3214:
83 GAG CGA TCA GGG TAG CGG TTC CTC CAG CGG TAG CCA CAG CTC OCT GCA OCT TGT TAG CAG GAC AAG CCT
TAC AGC GAG AAG ATC CAG CCT GG
- 3215:
84 GAA CCG CTA CCC TGA TCG CTC AGT GTG CTC TGG AGT GTC CTG CTG GAA CCG TGC TGA CCG ACG GAA CCA
CCT CTA CCT ACA AGC AGG CTG CTT C
- 3216:
85 GGT GTC GAT TCC AGC CAC CCA GTC GGT CTG CTT GGT GGT GTA GAA GTT AGC AGC ACA CTT CAC ACA CTC
AGA AGC AGC CTG CTT GTA GGT AG
- 3217:
86 GGG TGG CTG GAA TCG ACA OCT GTA CCT CTT GTA ACA AGA AGC TGA OCT CTG GAG CTG AGG CTA ACC TGC
CTG AGT CTG CTA AGA AGA ACA TC
- 3218:
87 GAG GGA TCC TTA TTA CAG CAG GTA AGA GAT CAG CAG CAG AGA GAT AGA CAG GAA GTT AGC GAA GTC
ACA CTG GAT GTT CTT CTT AGC AGA CT

Fig. 12

REPLACEMENT SHEET

17/27

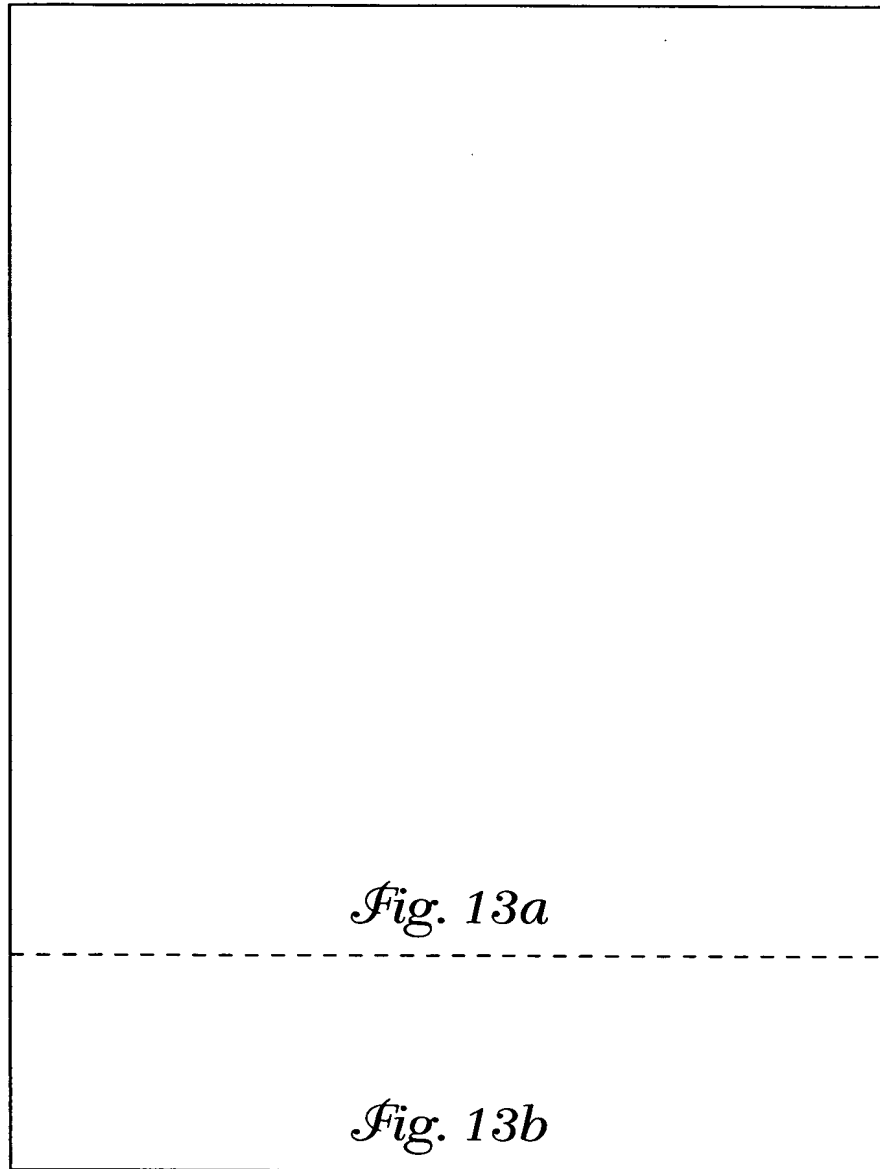
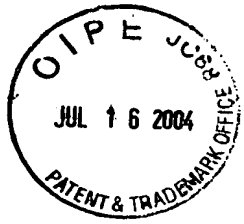
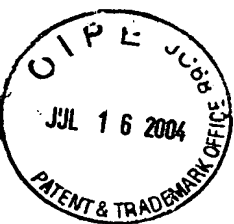


Fig. 13



G5 proline mutant 18/27

SEQ ID NO: 53

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70	80	90	100	110	120
GCTAACTGTC	CTGTGGGAAC	CGAGACCAAC	ACCGCTGGAC	AGGTGGACGA	CCTGGGAACC
130	140	150	160	170	180
CCTGCTAACT	GTGTGAAGTG	TCAGAAGAAC	TTCTACTACA	ACAACGCTGC	TGCTTTTCGTG
190	200	210	220	230	240
CCTGGAGCTT	CTACCTGTAC	CCCTTGTCCT	CAGAAGAAGG	ACGCTGGAGC	TCAGCCTAAC
250	260	270	280	290	300
CCTCCTGCTA	CCGCTAACCT	GGTGACCCAG	TGTAACGTGA	AGTGTCTCTGC	TGGAACCGCT
310	320	330	340	350	360
ATCGCTGGAG	GAGCTACCGA	CTACGCTGCT	ATCATCACCG	AGTGTGTGAA	CTGTGCGCATC
370	380	390	400	410	420
AACTTCTACA	ACGAGAACGC	TCCTAACTTC	AACGCTGGAG	CTTCTACCTG	TACCGCTTGT
430	440	450	460	470	480
CCTGTGAACC	GTGTGGGAGG	AGCTCTGACC	GCTGGAAACG	CTGCTACCAT	CGTGGCTCAG
490	500	510	520	530	540
TGTAACGTGG	CTTGTCTTAC	CGGAACCGCT	CTGGACGACG	GAGTGACCAC	CGACTACGTG
550	560	570	580	590	600
CGCTCTTTCA	CCGAGTGTGT	GAAGTGTGCG	CTGAACCTCT	ACTACAACGG	AAACAACGGA
610	620	630	640	650	660
AACACCCCTT	TCAACCCTGG	AAAGTCTCAG	TGTACCCCTT	GTCTTGCTAT	CAAGCCTGCT
670	680	690	700	710	720
AACGTGGCTC	AGGCTACCTT	GGGAAACGAC	GCTACCATCA	CCGCTCAGTG	TAAAGTGGCT
730	740	750	760	770	780
TGTCCTGACG	GAACCATCTC	TGCTGCTGGA	GTGAACAAC	GGGTGGCTCA	GAACACCGAG
790	800	810	820	830	840
TGTACCAACT	GTGCTCCTAA	CTTCTACAAC	AACAACGCTC	CTAACTTCAA	CCCTGGAAAC
850	860	870	880	890	900
TCTACCTGTC	TGCCTTGTC	TGCTAACAAG	GACTACGGAG	CTGAGGCTAC	CGCTGGAGGA
910	920	930	940	950	960
GCTGCTACCC	TGGCTAAGCA	GTGTAACATC	GCTTGTCTCTG	ACGGAACCGC	TATCGCTTCT
970	980	990	1000	1010	1020
GGAGCTACCA	ACTACGTGAT	CCTGCAGACC	GAGTGTCTGA	ACTGTGCTGC	TAACTTCTAC
1030	1040	1050	1060	1070	1080
TTCGACGGAA	ACAACTTCCA	GGCTGGATCT	TCTCGCTGTA	AGGCTTGTCC	TGCTAACAAG
1090	1100	1110	1120	1130	1140
GTGCAGGGAG	CTGTGGCTAC	CGCTGGAGGA	ACCGCTACCC	TGATCGCTCA	GTGTGCTCTG
1150	1160	1170	1180	1190	1200
GAGTGTCTCTG	CTGGAACCGT	GCTGACCGAC	GGAACCACTT	CTACCTACAA	GCAGGCTGCT
1210	1220	1230	1240	1250	1260
TCTGAGTGTG	TGAAGTGTGC	TGCTAACTTC	TACACCACCA	AGCAGACCGA	CTGGGTGGCT

Fig. 13a

REPLACEMENT SHEET

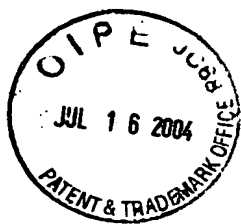
19/27



proline mutant

1270 1280 1290 1300 1310 1320
GGAATCGACA CCTGTACCTC TTGTAACAAG AAGCTGACCT CTGGAGCTGA GGCTAACCTG
1330 1340 1350 1360 1370 1380
CCTGAGTCTG CTAAGAAGAA CATCCAGTGT GACTTCGCTA ACTTCCTGTC TATCTCTCTG
1390 1400 1410 1420 1430 1440
CTGCTGATCT CTTACTACCT GCTG.....

Fig. 13b



20/27

G5 proline mutant protein

	↓	10	20	30	40	50	60
SEQ ID NO: 54		MKNNIPVILI	ISLFINQIKS	ANCPVGTETN	TAGQVDDLGT	PANCVNCQKN	FYYNNAAAFV
		70	80	90	100	110	120
		PGASTCTPCP	QKKDAGAQPN	PPATANLVTQ	CNVKCPAGTA	IAGGATDYAA	IITECVNCRI
		130	140	150	160	170	180
		NFYNNENAPNF	NAGASTCTAC	PVNRVGGALT	AGNAATIVAQ	CNVACPITGA	LDDGVTTDYV
		190	200	210	220	230	240
		RSFTECVKCR	LNFYNGNG	NTPFNPQKSQ	CTPCPAIKPA	NVAQATLGND	ATITAQCINVA
		250	260	270	280	290	300
		CPDGTISAAG	VNNWVAQNT	CTNCAPNFYN	NNAPNFNPGN	STCLPCPANK	DYGAEATAGG
		310	320	330	340	350	360
		AATLAKQCNI	ACPDGTAIAS	GATNYVILQT	ECLNCAANFY	FDGNNFQAGS	SRCKACPANK
		370	380	390	400	410	420
		VQGAVATAGG	TATLIAQCAL	ECPAGTVLTD	GTTSTYKQAA	SECVKCAANF	YTTKQTDWVA
		430	440	450	460	470	480
		GIDTCTSCNK	KLTSGAEANL	PESAKNMQC	DFANFLSISL	LLISYYLL..

Fig. 14



21/27

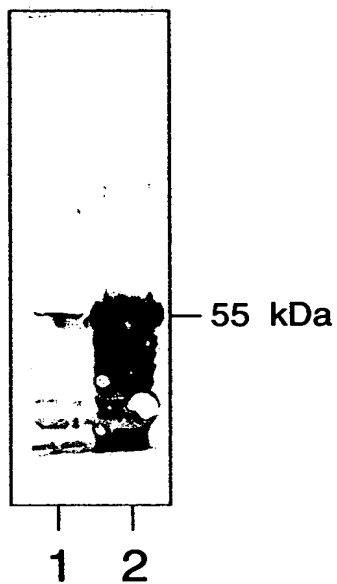


Fig. 15

22/27

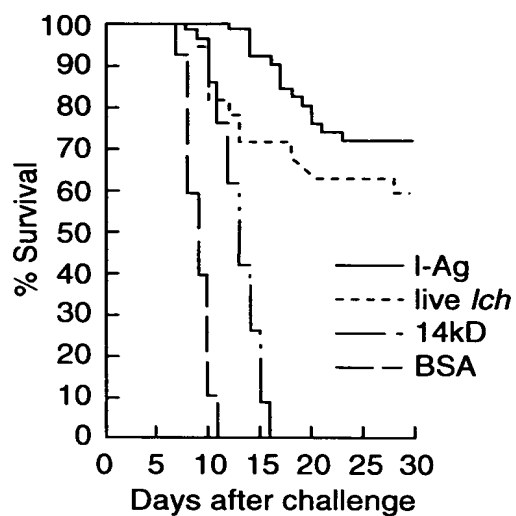


Fig. 16

23/27

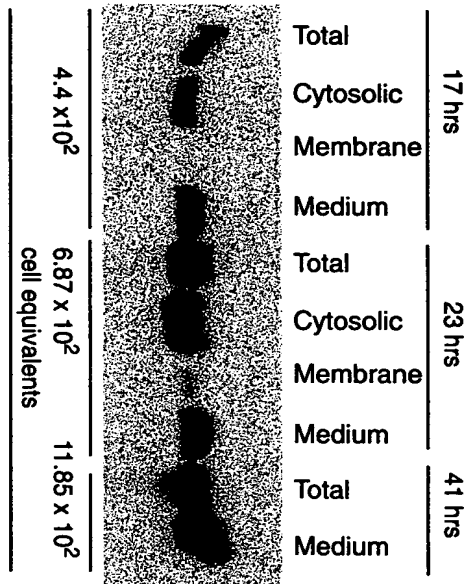


Fig. 17

REPLACEMENT SHEET

24/27

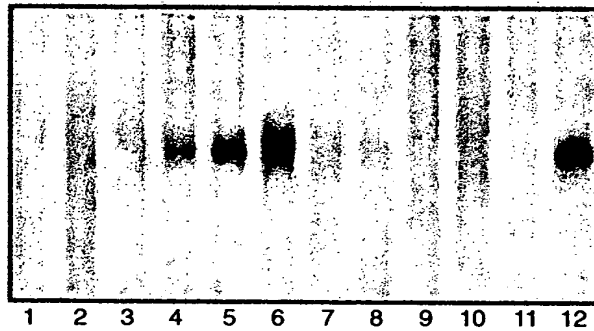


Fig. 18

REPLACEMENT SHEET



25/27

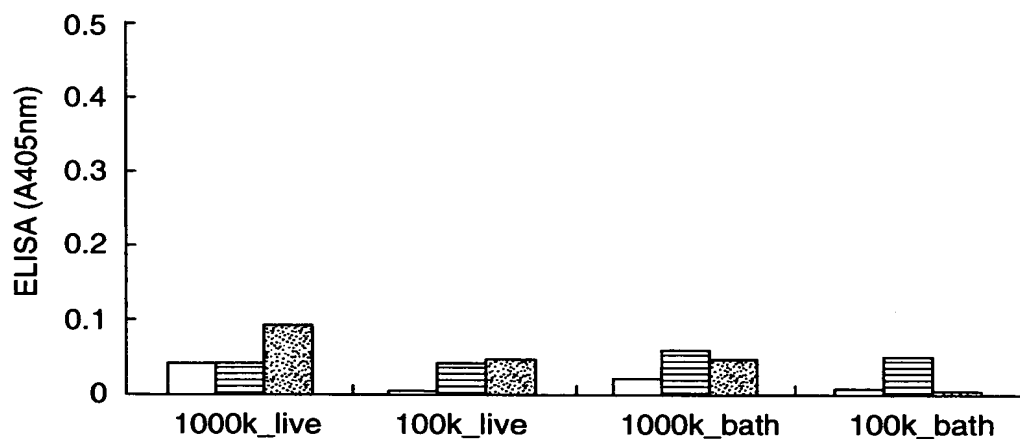


Fig. 19a

□ Week 2
 ▨ Week 4
 ▩ Week 6

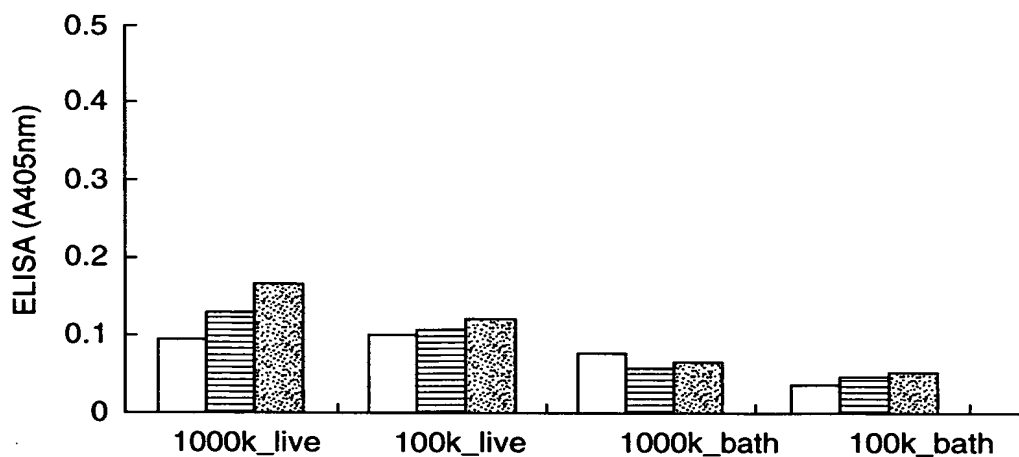
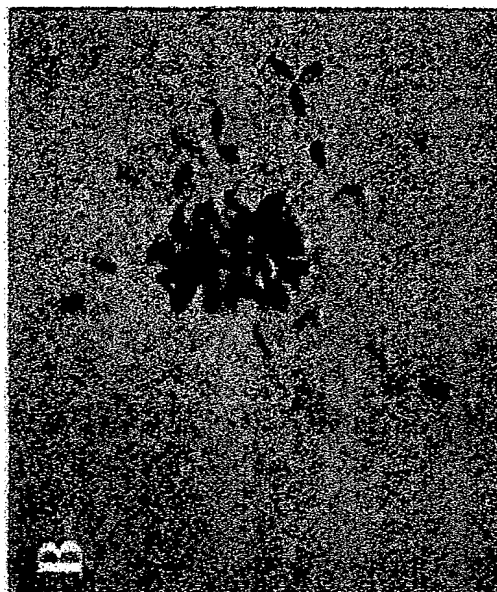


Fig. 19b

□ Week 2
 ▨ Week 4
 ▩ Week 6

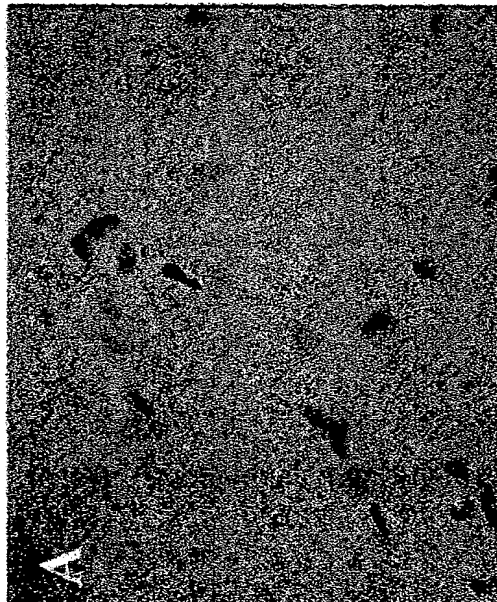
REPLACEMENT SHEET

26/27



Serum: anti-live TG1 (1 : 20)

Fig. 20b



Serum: anti-live Tneo (1 : 20)
(negative control)

Fig. 20a



27/27

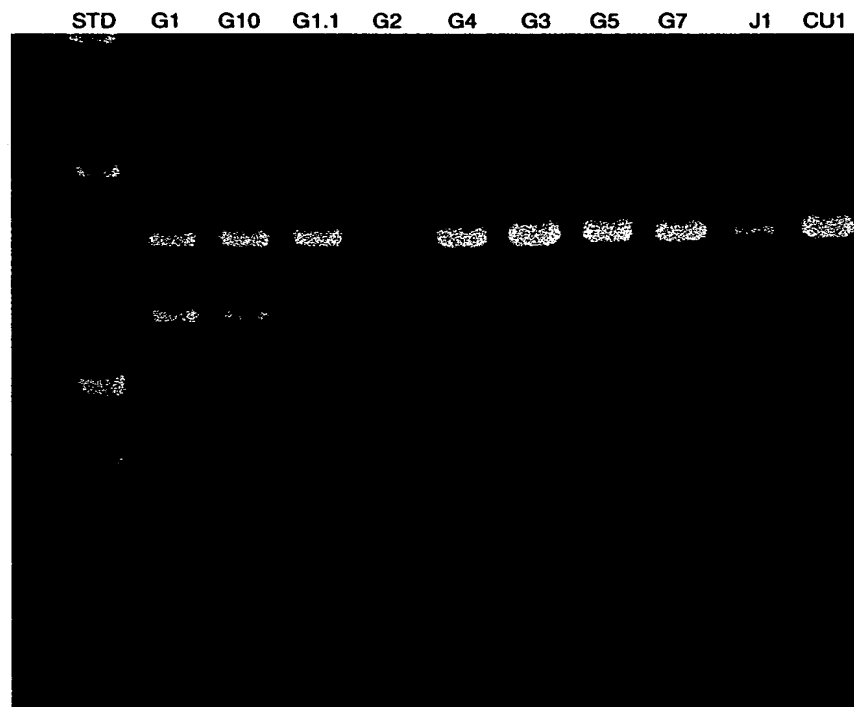


Fig. 21